

end by two adjacent sequence regions, and a first tag that is designed not to hybridize to said adjacent sequence regions when the first target-specific portion is sequence specifically hybridized to the first target nucleic acid sequence; and

a first mobility-modifier comprising a first tail and a first tag complement for binding to the first tag; and

a second complex comprising:

C¹
cont
a second probe comprising a second target-specific portion for sequence-specific hybridization to a second target nucleic acid sequence that is flanked at each end by two adjacent sequence regions, and a second tag that is designed not to hybridize to the second said adjacent sequence regions when the second target-specific portion is sequence specifically hybridized to the second target nucleic acid sequence; and

a second mobility-modifier comprising a second tail and a second tag complement for binding to the second tag;

wherein a mobility of the first complex in a mobility-dependent analysis technique is distinguishable from a mobility of the second complex in the mobility-dependent analysis technique; and

wherein the first complex and the second complex are present as a mixture.

REMARKS

With reference to the Office action mailed May 9, 2002, reconsideration of the application is respectfully requested. Claim 1 has been amended. Claims 1-12 are pending.

I. Amendments

Claim 1 has been amended to recite that the first probe comprises a first target-specific portion for sequence-specific hybridization to a first target nucleic acid sequence that is flanked at each end by two adjacent sequence regions, and a first tag that is designed not to hybridize to said adjacent sequence regions when the first target-specific portion is sequence specifically hybridized to the first target nucleic acid sequence. Similar amendments have been made to the description of the second probe in the second complex.

Support can be found in Fig. 4C, for example, which illustrates exemplary complexes encompassed by claim 1 which are sequence-specifically hybridized to different target sequences